

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/532,746
PCT
6/14/05

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/537,746

DATE: 06/14/2005
TIME: 09:17:55

Input Set : A:\01-SQ Listing-06 Jun 2005.txt
Output Set: N:\CRF4\06142005\J537746.raw

3 <110> APPLICANT: De Maria, Leonardo
4 Svendsen, Allan
5 Borchert, Torben Vedel
6 Christensen, Lars Lehmann Hylling
7 Larsen, Sine
8 Ryttergaard, Carsten
10 <120> TITLE OF INVENTION: Galactanase Variants
12 <130> FILE REFERENCE: 10319.204-US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/537,746
C--> 14 <141> CURRENT FILING DATE: 2005-06-06
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: PatentIn version 3.3

Does Not Comply
Corrected Diskette Needed

(Pg. 2-3)

ERRORED SEQUENCES

645 <210> SEQ ID NO: 9
646 <211> LENGTH: 359
647 <212> TYPE: PRT
648 <213> ORGANISM: Pseudomonas fluorescens
651 <220> FEATURE:
652 <221> NAME/KEY: mat_peptide
653 <222> LOCATION: (1)..()
655 <400> SEQUENCE: 9
657 Asn Thr Gly Val Ala Asp Asn Thr Pro Phe Tyr Val Gly Ala Asp Leu
658 1 5 10 15
661 Ser Tyr Val Asn Glu Met Glu Ser Cys Gly Ala Thr Tyr Arg Asp Gln
662 20 25 30
665 Gly Lys Lys Val Asp Pro Phe Gln Leu Phe Ala Asp Lys Gly Ala Asp
666 35 40 45
669 Leu Val Arg Val Arg Leu Trp His Asn Ala Thr Trp Thr Lys Tyr Ser
670 50 55 60
673 Asp Leu Lys Asp Val Ser Lys Thr Leu Lys Arg Ala Lys Asn Ala Gly
674 65 70 75 80
677 Met Lys Thr Leu Leu Asp Phe His Tyr Ser Asp Thr Trp Thr Asp Pro
678 85 90 95
681 Glu Lys Gln Phe Ile Pro Lys Ala Trp Ala His Ile Thr Asp Thr Lys
682 100 105 110
685 Glu Leu Ala Lys Ala Leu Tyr Asp Tyr Thr Asp Thr Leu Ala Ser
686 115 120 125
689 Leu Asp Gln Gln Leu Leu Pro Asn Leu Val Gln Val Gly Asn Glu
690 130 135 140
693 Thr Asn Ile Glu Ile Leu Gln Ala Glu Asp Thr Leu Val His Gly Ile

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/537,746

DATE: 06/14/2005
TIME: 09:17:55

Input Set : A:\01-SQ Listing-06 Jun 2005.txt
Output Set: N:\CRF4\06142005\J537746.raw

694 145 150 155 160
697 Pro Asn Trp Gln Arg Asn Ala Thr Leu Leu Asn Ser Gly Val Asn Ala
698 165 170 175
701 Val Arg Asp Tyr Ser Lys Lys Thr Gly Lys Pro Ile Gln Val Val Leu
702 180 185 190
705 His Ile Ala Gln Pro Glu Asn Ala Leu Trp Trp Phe Lys Gln Ala Lys
706 195 200 205
709 Glu Asn Gly Val Ile Asp Tyr Asp Val Ile Gly Leu Ser Tyr Tyr Pro
710 210 215 220
713 Gln Trp Ser Glu Tyr Ser Leu Pro Gln Leu Pro Asp Ala Ile Ala Glu
714 225 230 235 240
717 Leu Gln Asn Thr Tyr His Lys Pro Val Met Ile Val Glu Thr Ala Tyr
718 245 250 255
721 Pro Trp Thr Leu His Asn Phe Asp Gln Ala Gly Asn Val Leu Gly Glu
722 260 265 270
725 Lys Ala Val Gln Pro Glu Phe Pro Ala Ser Pro Arg Gly Gln Leu Thr
726 275 280 285
729 Tyr Leu Leu Thr Leu Thr Gln Leu Val Lys Ser Ala Gly Gly Met Gly
730 290 295 300
733 Val Ile Tyr Trp Glu Pro Ala Trp Val Ser Thr Arg Cys Arg Thr Leu
734 305 310 315 320
737 Trp Gly Lys Gly Ser His Trp Glu Asn Ala Ser Phe Phe Asp Ala Thr
738 325 330 335
741 Arg Lys Asn Asn Ala Leu Pro Ala Phe Leu Phe Phe Lys Ala Asp Tyr
742 340 345 350
745 Gln Ala Ser Ala Gln Ala Glu
746 355
E--> 752 1

pls delete

10/537,746

Page 3

<210> 5
<211> 21
<212> DNA
<213> synthetic

INVALID
Response

<220>
<221> misc_feature
<223> Primer

<400> 5
catttggaca acggctggag c

↑
pls see item # 10
on error
summary sheet

Mandatory,
<213> response
has to be either
Artificial,
Unknown or
Genus species,

21

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/537,746

DATE: 06/14/2005

TIME: 09:17:56

Input Set : A:\01-SQ Listing-06 Jun 2005.txt
Output Set: N:\CRF4\06142005\J537746.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:752 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/537,786

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the **only valid** <213> responses are: **Unknown, Artificial Sequence, or scientific name (Genus/species)**. <220>-<223> section is **required** when <213> response is **Unknown** or is **Artificial Sequence**
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" **can only represent a single nucleotide**; "Xaa" **can only represent a single amino acid**